Figure 1A

-	comuna su si sis nana a saintiga accanaulati ne saa neeb cadacti codadadaa accadi	ē.
51	Tacascructus acranas sociascrructana na processo da corotora.	* * ·
	ATGGETETGGGGACAGGACAGGTGGATTACCCAACGGGGGGGGGG	44 C)
221	GGOTOOTOOTOOTOOGOGGAGOOGOTUTTOUCOOACATOGTGGAGOTGAACGTG 3 S S S S A E P P L F P D I V E L N V	040
241	GGGGGCAGSTGTACGTGACCGGGGGTGCACGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	300 60
301 61	TGGCGCATGTTCACGCAGCAGCAGCAGCAGGAGCAGCAAAGGCCGCTTC W R M F T Q Q Q P Q E L A F D S K G F F	3.60 80
361 81	TTTCTGGACGGGACGGCTTCCTCTTCCGCTACATCCTGGATTACCTGCGGGACTTGCAG F L D R D G F L F R Y I L D Y L R D L Q	420 100
421 101	CTOGTGCTGCCGACTACTTCCCCGAGCGGAGCCGGGCTGCAGCGGGGGGGG	480 130
481 121	GAGCTGCCAGAGCTCGTGCGCCGCCCTCGGGGGCCCGGGGGCCGCCGGGGGCCGCC	540 140
541 141	CCCTCGCGGCGCGGGTGCACAAGGAGGCTCGCTGGGTGACGAGCTGCTGCCGCTTGGC PSRRGVHKEGSSLGDELLPLG	600 1 60
601 161		660 180
661 181	OTBSCTAGECGAGTCCGGGGGGGGGGGGGGGGGGGGGGGGGGGG	720 200
	CTGGACGGCAGCGGCTCGGGCTACACCATCACCATCGGCTACCGCGGGCTCCTACACCATC	
		640 240
441 141	AABABBT SENTER SUNAA BEAR ESTETTT BEGGA CA CONTEXABBAAA GCCGGGGACCCCGAC KOTOS LAKEEN FBOTT LEES ES EDPD	911 241

Figure 1B

9.1 161	not noone slages taleachet eiges et af tanet eaagt teaaet teef is aagtaggee B. P. P. B. B. Y. T. S. B. Y. Y. L. B. B. M. F. L. B. L. A.	980 240
961 281	TTUGACAAGUTSTAGGAGTTGGGAGATGGTGGGGTGAGGTUAAGGGGGGGTGG F D K L S E S G F H M V A C S S T G T C	300
1021		1090 320
1091 321	GT PTTOTOCAGO SA STGA SET PODOCAGA DUCO OT PODOCA OT PODA GA PROCETTOTO VIENE CIENTA EL EL CONTROL DE LA CONTROL DE LA CONTROLA DEL CONTROLA DE LA CONTROLA DE LA CONTROLA DE LA CONTROLA DE LA CONTROLA DEL CONTROLA DE LA CONTROLA DEL CONTROLA DEL CONTROLA DEL CONTROLA DE LA CONTROLA DEL CO	1140 325
1141	CTGCCCGAGAGATGATTACAGAGCCTCTTGTCCCACCTTTGTCCCCTGGCTGCTGCCCTC	1200
1201		1260
1261	AGAACCT3CAGCCGCAAATCCTCTGGGCT3CTTCGTCTTTTGGACCTCCTGAACCGAG	1320
1321	AGAACCCAGAGGAACCCCACCCCACCCACCTACCACTCCATGCTTTCTCTACTCCCT	1380
1381	GCCTCAAACCACCCCTCCCCCAGATGGTACTTCAGTTTGGATCTATTGGGGGAGTGTGGC	1440
1441	CACAGACCGGGGGATGATTGAATTGTTCAGAACCTGATTGGACCGTGTCCAATGTGCGGA	1500
1501		1560
1561		1620
1621		1680
1681		1740
1741		1800
1911	TGTGCGGAAGATTTCCTTGAAATCTTCTCAAGCTCTTATGACTCACTGGGGGTTTAAGAG	1960
14/1	AT WARRANT SOTT NYARTOT YT ROGETTAGTETTTTAGAAGGTGATTAGAGAGTGTTTTT	1920
	GACCTOTTTTGAAGGTAGAGTTTTAGAAGGTGGGAAGATTTTGAGAGGTGGAAGATTTTGAG	1980

Figure 1C

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			TTTT JAAAA 31	

10.41 AAAAAAAAAAA 1.51

Figure 2A

		51
E+betaMi		MALALUTEGUPNGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
roime i	1.1	MNKKLUMA, KRIJETR A LILI J V TM VV CAV I TY Y ILV TT VL
K+Hncv27		MSEFLITESPASPLKN, SIPTPA, LTESNAP <mark>VHIDWGGHMYTSSLA</mark>
H+Hnov2+	-	MDN JEW JYMMIDP <mark>V</mark> DLNVGGHLYTTSLT
riaalli		L. KKSTMALSEN CORYYPREJEST INNOFPEVYBLNWGGOVYFTRHS
3310465		
331033		MPEIIEMNGGUSWATTLA
H+channel tetra		MTSVEDVITLN'GGTMYTTTRS
n-channel_tella	! = !	
		51 100
K+betaM6	(51)	TVVS::PDSLL::::::::::::::::::::::::::::::::
n+Decard KCIMEl	(40)	PLYQESUNTQESKCHLIETNIRDQEELKGKKUPQYPCLWVNVSAAGRWAV
K+Hnav27	(47)	TKY PESRIGRLED TEPIVLDSLKCHYFIDRDCOMFRYILL FI
K+Hnc+124	(29)	TRYPDSMCGAMEGEOFPTARDPQENYFIDRDGPLERYVENFI
KIAA1317	(49)	TLISIPHSLLWEMESPERDTANDLAKDSKCRFFIDRDCFLFRYILDYL
CG10465	(36)	TVTKNNDTMISAMFSCRMEVLTDSECWILIDRCSNHFGIILNYL
CG10330	(20)	TLLQDKSTLLAELFGEGRDSLAKDSKGRYFLDRDGVLFRYILDFL
K+channel_tetra	(23)	TLSKETDTULANIASCSLSEDEÇANVVTLPDCTLFVDRDGPLFAYVLHFL
		101
** 1 :	,	101 150
K+betaM6	(97)	RDLQLVLPDYFPERSRLQREAEYFELPELVRRLGAPQQPGPGPPPSRRGV
KCNMB1	(90)	LYHTEDTRDQNQQCSYIPGSVDNYQTAFADVEKVRAKFQEQQ
K+Hnow27	(92)	RTSKULIPDDEKDYTLLYBEAKYFOLOPMLLEMERWKODRET
K+Hnov23	(73)	RTSDITLPLIPKDFDLLRKEADFYQIEFLIQCLNDPKPLYP
KIAA1317	(∃₹)	RDRQVVIPDHAPDKGRUKREMEMFQUPILVKLUTPDEIKQSP
CG10465	(80)	RDGTVPLPETNKBIABILABAKYYCITELAISCERALYAHQEPKPICRIP
CG10830	(65)	RDKADHUPEGERERQRILREAEHFKITAMLECIRSERDARP
K+channel_tetra	(~3)	RTDKISLPEÇEREVARIKDEADFYRIEFFSTLISNASSISP
		151 230
K+betaM6		151 200 HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGAAGPLLT
KCNMB 1	(1:1)	
KCNME 1 K+Hnow2 7	(131) (134)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGAAGPLLT
KCNMB1 K+Hnow2 7 K+Hnow2 3	(1:1) (1:4) (1:4)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGAAGPLLT
KCNMB1 K+Hnow27 K+Hnow28 KIAA1317	(1:1) (1:4) (1:4) (1:9)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGAAGPLLT
KCNMB1 K+Hnov27 K+Hnov23 KIAA1317 CG10465	(1:1) (1:4) (1:4) (1:9) (1:0)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGAAGPILTDEFCHSDFEDASQGSDTRICP LITSQKEEQLLLSVSLKPAVILVVQRQNNKYSYTSTS
KCNME1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830	(100) (104) (114) (119) (110) (106)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGAAGPILTDEFCHSDFEDASQGSDTRICP LITSQKEEQLLLSVSLKPAVILVVQRQNNKYSYTSTS
KCNMB1 K+Hnov27 K+Hnov23 KIAA1317 CG10465	(1:1) (1:4) (1:4) (1:9) (1:0)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGAAGPILTDEFCHSDFEDASQGSDTRICP LITSQKEEQLLLSVSLKPAVILVVQRQNNKYSYTSTS
KCNME1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830	(100) (104) (114) (119) (110) (106)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGAAGPILTDEFCHSDFEDASQGSDTRICP LITSQKEEQLLLSVSLKPAVILVVQRQNN
KCNME1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 K+channel_tetra	(111) (114) (114) (119) (110) (106) (114)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGAAGPILT DEFCHSDFEDASQ
KCNME1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG1383) K+channel_tetra K+betaM6	(191) (194) (114) (119) (110) (106) (114)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGAAGPILT DEFCHSDFEDASQGSDTRICP LITSQKEEQLLLSVSLKPAVILVVQRQNNKYSYTSTS
KCNME1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 K+channel_tetra K+betaM6 KCNMB1	(191) (194) (114) (119) (120) (106) (114) (197) (132)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASFSPSGGAAGPLLT DEFCHSDFEDASQ
KCNME1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 K+channel_tetra K+betaM6 KCNMB1 K+Hnow27	(191) (194) (114) (119) (110) (1106) (114) (197) (132) (134)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASFSPSGGAAGPLLT DEFCHSDFEDASQ
KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10466 CG10830 K+channel_tetra K+betaM6	(191) (194) (114) (119) (110) (106) (114) (197) (132) (134) (114)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASF.SPSGGAAGPLLT DEFCHSDFEDASQ
KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 K+channel_terra K+betaM6 KCNMB1 K+Hnow27 K+Hnow28 KIAA1317	(192) (194) (114) (119) (190) (196) (114) (197) (132) (134) (114) (160)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASFSPSGGAAGPLLT DEFCHSDFEDASQGSDTRICP LITSQKEEQLLLSVSLKPAVILVVQRQNNKYSYTSTS
KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG1083) K+channel_tetra K+betaM6 KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465	(100) (104) (114) (119) (110) (110) (114) (120) (134) (114) (160) (167)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASF.SPSGGAAGPILT DEFCHSDFEDASQGSDTRICP LITSQKEEQLLLSVSLKPAVILVVQRQNNKYSYTSTS
KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG1083) K+channel_terra K+betaM6 KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830	(191) (194) (114) (119) (120) (106) (114) (197) (132) (134) (114) (160) (167) (107)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASF.SPSGGAAGPILT DEFCHSDFEDASQGSDTRICP LITSQKEEQLLLSVSLKPAVILVVQRQNNKYSYTSTS
KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG1083) K+channel_tetra K+betaM6 KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465	(191) (194) (114) (119) (120) (106) (114) (197) (132) (134) (114) (160) (167) (107)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASF.SPSGGAAGPILT DEFCHSDFEDASQGSDTRICP LITSQKEEQLLLSVSLKPAVILVVQRQNNKYSYTSTS
KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG1083) K+channel_terra K+betaM6 KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830	(191) (194) (114) (119) (120) (106) (114) (197) (132) (134) (114) (160) (167) (107)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASF.SPSGGAAGPLLT DEFCHSDFEDASQGSDTRICP LITSQKEEQLLLSVSLKPAVILVVQRQNNKYSYTSTS
KCNMB1 K+Hnov27 K+Hnov28 KIAA1317 CG10465 CG10830 K+channel_tetra K+betaM6 KCNMB1 K+Hnov27 K+Hnov28 KIAA1317 CG10465 CG10830 K+channel_tetra	(191) (194) (114) (119) (120) (106) (114) (197) (132) (134) (114) (160) (167) (107) (121)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASF.SPSGGAAGPILT DEFCHSDFEDASQGSDTRICP LITSQKEEQLLLSVSLKPAVILVVQRQNNKYSYTSTSPRTANG 261 PSQSLDGSRRSCYITIGYRGSYTIGRDAQADAKFRRVARITVCGKTSLAKVFYCFSAPRGNETSVLFQRLYGPQALLFSLFWPTFLLTGGLL
KCNME1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 K+channel_tetra K+betaM6 KCNMB1 K+Hnow27 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 E+channel_tetra K+betaM6	(191) (194) (114) (119) (120) (106) (114) (197) (122) (134) (160) (167) (107) (121)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASF.SPSGGAAGPILT DEFCHSDFEDASQGSDTRICP LITSQKEEQLLLSVSLKPAVILVVQRQNNKYSYTSTS
KCNME1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 K+channel_tetra K+betaM6 KCNMB1 K+Hnow27 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 K+channel_tetra K+betaM6 KCNMB1	(191) (134) (114) (119) (110) (110) (114) (132) (134) (114) (160) (167) (107) (121) (247) (174)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASESPSGAAGPLLT DEFCHSDFEDASQ
KCNMB1 K+Hnov27 K+Hnov28 KIAA1317 CG10465 CG10830 K+channel_tetra K+betaM6 KCNMB1 K+Hnov27 K+Hnov27 K+Hnov28 KIAA1317 CG10465 CG10830 E+channel_tetra K+betaM6 KCNMB1 K+Hnov27	(191) (134) (114) (119) (110) (110) (114) (121) (132) (134) (114) (160) (167) (107) (121) (174) (173)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASESPSGAAGPLLT DEFCHSDFEDASQ
KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 K+channel_tetra K+betaM6	(191) (194) (114) (119) (190) (106) (114) (197) (132) (134) (114) (160) (167) (107) (121) (174) (173) (174) (173) (154)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASFSPSGAAGPLLT DEFCHSDFEDASQ
KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG1083) K+channel_terra K+betaM6 KCNMB1 K+Hnow27 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 E+channel_terra K+betaM6 KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830	(192) (134) (114) (119) (130) (106) (114) (197) (132) (134) (114) (160) (167) (107) (121) (247) (174) (174) (154) (210)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASF.SPSGGAAGPLLT
KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 K+channel_terra K+betaM6 KCNMB1 K+Hnow27 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 E+channel_terra K+betaM6 KCNMB1 K+Hnow17 K+Hnow17 CH10465 CG10830	(191) (194) (114) (119) (110) (106) (114) (197) (182) (134) (114) (160) (167) (107) (121) (247) (174) (173) (174) (173) (115) (117)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASF.SPSGGAAGPLLT
KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 K+channel_terra K+betaM6 KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 E+channel_terra K+betaM6 KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830	(192) (134) (114) (119) (130) (106) (114) (197) (132) (134) (114) (160) (167) (107) (121) (247) (173) (174) (173) (154) (210) (146)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASF.SPSGGAAGPLUT
KCNMB1 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 K+channel_terra K+betaM6 KCNMB1 K+Hnow27 K+Hnow27 K+Hnow28 KIAA1317 CG10465 CG10830 E+channel_terra K+betaM6 KCNMB1 K+Hnow17 K+Hnow17 CH10465 CG10830	(192) (134) (114) (119) (130) (106) (114) (197) (132) (134) (114) (160) (167) (107) (121) (247) (173) (174) (173) (154) (210) (146)	HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASFSPSGAAGPLUT



		35.
H. Fest aMi	12961	STRICAFASUT: -D. SEDKIWISYIEWWECKE
rome i	1927	
H+Hm:v2 ⁿ	12001	GG FYDSSIFLHYVLRRELRRTPRVPAVIRIHIEFL
H+Hn:v2+	. 1141	TIRNTENHEMOREANENTNEHNWIF GLARMIDI
22AA1317	12591	SCUTASEINWYTDDKIWSSYTEYUFYREFCEWGFGHOLOGUENGE
2 ¥1 0 4 0 5	12671	VGSASGTSIM, YTSDEEERTGLARLRSMARUNPD
0310930	(196)	GSGTAGSAAEPHPGVDTEENRWNHYNEFVFIRD
K+channel_tetra	(141)	
		351 400
K+betaM6	(326)	
FCNMB1	(192)	
K+Hnov27	(257)	
E+Hncv28	(233)	
KIAA1317	(3.34)	GDKEGESGTSCHDLSTSSCDSQSEASSPQETWIGGPVTRQTHIQTLDRPI
CG10465	(302)	
CG10830	(229)	
K+channel_tetra	(141)	
		401 450
K+betaM6	(325)	
KCNMB1	(192)	
K+Hnov27	(257)	
K+Hnov28	(233)	
KIAA1317	(354)	KKGPVQLIQQSEMRRKSDLLRTLTSGSRESNMSSKKKAVKEKLSIEEELE
CG10465	(302)	
CG10830	(219)	
K+channel_tetra	(141)	
		451 482
H+betaM6	(315)	
KCMMB1	(191)	
K+Hncv27	(257)	
K+Hnov28	(238)	
KIAA1317	(404)	KCIQDFLKIKIPDRFPERKHPWQSELLRKYHL
CG10465	(302)	
CG10830	(229)	
K+channel_tetra	(141)	

Figure 3

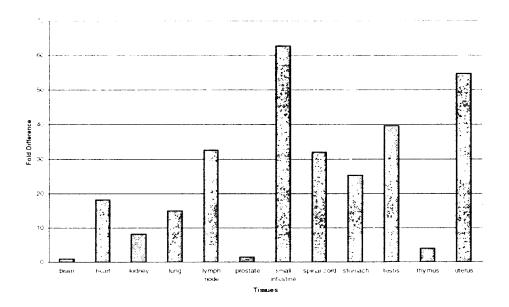
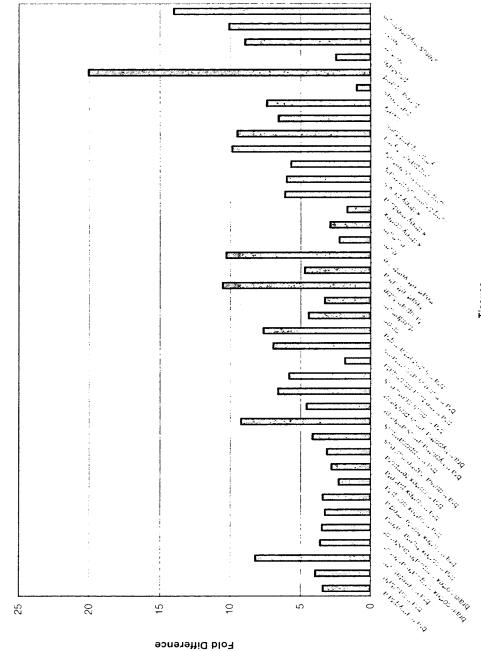


Figure 4.

<u>Protein</u>	Genbank / SWISS- PROT	<u>Identities</u>	Similarities	
	Accession No.			
human Maxi-K potassium channel beta subunit, KCNMB1 protein	gil4758625	0.0%	37.5%	
human potassium channel K+Hnov27 protein	gilY34125	30.21%	39.15%	
human potassium channel K+Hnov28 protein	gilY34129	30.04%	38.63%	
Caenorhabditis elegans K+ channel tetramerisation domain containing protein	gil3880445	31.116	39.26%	
Drosophila CG10465 protein	gil17946205	23.9%	33.0%	
Drosophila CG10830 protein	gil7300672	50.89°c	62.5%	
human KIAA1317 protein	gil7243015	60.42%	69.97%	

Figure 5



Tissues